I.   Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.17 [Jun-24-2007]
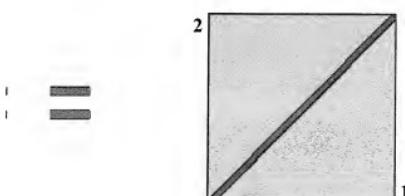
Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]

x_dropoff: [0] expect: [10.00] wordsize: [3] Filter ☑ View option [Standard ▼]

Masking character option [X for protein, n for nucleotide ▼] Masking color option

[Black ▼]

☐ Show CDS translation [Align]

Sequence 1: lcl|1
Length = 116 (1 .. 116)

Sequence 2: lcl|65536
Length = 116 (1 .. 116)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  261 bits (666),  Expect = 1e-68
 Identities = 115/116 (99%), Positives = 115/116 (99%), Gaps = 0/116 (0%)

Query  1    SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASWRNSSGTIELVKKGCW   60
            SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASW NSSGTIELVKKGCW
Sbjct  1    SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASW NSSGTIELVKKGCW   60

Query  61   LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT   116
            LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT
Sbjct  61   LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT   116

CPU time:     0.02 user secs.     0.01 sys. secs      0.03 total secs.
```